

## us-09-939-537-31\_copy\_1\_200.rup

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OM protein - protein search, using sw model

Run on: March 7, 2005, 06:56:21 ; Search time 75.9095 Seconds  
(without alignments)  
1349.183 Million cell updates/sec

Title: US-09-939-537-31\_COPY\_1\_200

Perfect score: 1029  
Sequence: 1 MNRGVPFERHLVLLVQLALP.....TWCTCTVLQNLQKVKFPIKIDIV 200

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512073187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03:  
1: uniprot\_sprot:  
2: uniprot\_trembl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match Length	DB	ID	Description
1	1023	99.4	458	1	CDA_HUMAN	PO1730 homo sapien
2	999	97.1	458	1	CDA_PANTR	P16004 pan troglod
3	912	88.6	458	1	CDA_MACPA	P79185 macaca fasc
4	910	88.4	458	1	CDA_MACFU	P79184 macaca fusc
5	904	87.9	458	1	CDA_MACMU	P16003 macaca mulatta
6	903	87.8	458	1	CDA_MACMU	Q08338 cercopithecus aethiops
7	885	86.0	458	1	CDA_CERAB	RX-MADDON, Littman D.R., Godfrey M., Maddon D.B., Chess L., Axel R.; "The isolation and nucleotide sequence of a cDNA encoding the T cell surface protein T4: a new member of the immunoglobulin gene family"; Cell 42:93-104(1985).
8	784	76.2	397	1	CDA_CERTO	RX-MADDON, Littman D.R., Godfrey M., Maddon D.B., Chess L., Axel R.; "The isolation and nucleotide sequence of a cDNA encoding the T cell surface protein T4: a new member of the immunoglobulin gene family"; Cell 42:93-104(1985).
9	783	76.1	397	1	CDA_BRYPA	RX-MADDON, Littman D.R., Godfrey M., Maddon D.B., Chess L., Axel R.; "The isolation and nucleotide sequence of a cDNA encoding the T cell surface protein T4: a new member of the immunoglobulin gene family"; Cell 42:93-104(1985).
10	767	74.5	397	2	Q0261	RX-MADDON, Littman D.R., Godfrey M., Maddon D.B., Chess L., Axel R.; "The isolation and nucleotide sequence of a cDNA encoding the T cell surface protein T4: a new member of the immunoglobulin gene family"; Cell 42:93-104(1985).
11	767	74.5	397	2	Q0262	RX-MADDON, Littman D.R., Godfrey M., Maddon D.B., Chess L., Axel R.; "The isolation and nucleotide sequence of a cDNA encoding the T cell surface protein T4: a new member of the immunoglobulin gene family"; Cell 42:93-104(1985).
12	767	74.5	397	2	Q0263	RX-MADDON, Littman D.R., Godfrey M., Maddon D.B., Chess L., Axel R.; "The isolation and nucleotide sequence of a cDNA encoding the T cell surface protein T4: a new member of the immunoglobulin gene family"; Cell 42:93-104(1985).
13	767	74.5	397	2	Q5NNE9	RX-MADDON, Littman D.R., Godfrey M., Maddon D.B., Chess L., Axel R.; "The isolation and nucleotide sequence of a cDNA encoding the T cell surface protein T4: a new member of the immunoglobulin gene family"; Cell 42:93-104(1985).
14	763	74.1	397	2	Q0259	RX-MADDON, Littman D.R., Godfrey M., Maddon D.B., Chess L., Axel R.; "The isolation and nucleotide sequence of a cDNA encoding the T cell surface protein T4: a new member of the immunoglobulin gene family"; Cell 42:93-104(1985).
15	763	74.1	397	2	Q0260	RX-MADDON, Littman D.R., Godfrey M., Maddon D.B., Chess L., Axel R.; "The isolation and nucleotide sequence of a cDNA encoding the T cell surface protein T4: a new member of the immunoglobulin gene family"; Cell 42:93-104(1985).
16	741.5	72.1	457	2	QBHZB	RX-MADDON, Littman D.R., Godfrey M., Maddon D.B., Chess L., Axel R.; "The isolation and nucleotide sequence of a cDNA encoding the T cell surface protein T4: a new member of the immunoglobulin gene family"; Cell 42:93-104(1985).
17	740.5	72.0	457	2	QBHZT	RX-MADDON, Littman D.R., Godfrey M., Maddon D.B., Chess L., Axel R.; "The isolation and nucleotide sequence of a cDNA encoding the T cell surface protein T4: a new member of the immunoglobulin gene family"; Cell 42:93-104(1985).
18	737.0	71.7	457	1	CDA_SAISC	RX-MADDON, Littman D.R., Godfrey M., Maddon D.B., Chess L., Axel R.; "The isolation and nucleotide sequence of a cDNA encoding the T cell surface protein T4: a new member of the immunoglobulin gene family"; Cell 42:93-104(1985).
19	598	58.1	463	1	CDA_CANFA	RX-MADDON, Littman D.R., Godfrey M., Maddon D.B., Chess L., Axel R.; "The isolation and nucleotide sequence of a cDNA encoding the T cell surface protein T4: a new member of the immunoglobulin gene family"; Cell 42:93-104(1985).
20	597	58.0	455	2	Q71QE2	RX-MADDON, Littman D.R., Godfrey M., Maddon D.B., Chess L., Axel R.; "The isolation and nucleotide sequence of a cDNA encoding the T cell surface protein T4: a new member of the immunoglobulin gene family"; Cell 42:93-104(1985).
21	592	57.5	455	2	Q9S78	RX-MADDON, Littman D.R., Godfrey M., Maddon D.B., Chess L., Axel R.; "The isolation and nucleotide sequence of a cDNA encoding the T cell surface protein T4: a new member of the immunoglobulin gene family"; Cell 42:93-104(1985).
22	587.5	57.1	459	1	CDA_RABIT	RX-MADDON, Littman D.R., Godfrey M., Maddon D.B., Chess L., Axel R.; "The isolation and nucleotide sequence of a cDNA encoding the T cell surface protein T4: a new member of the immunoglobulin gene family"; Cell 42:93-104(1985).
23	562	54.6	432	2	Q6LBKL	RX-MADDON, Littman D.R., Godfrey M., Maddon D.B., Chess L., Axel R.; "The isolation and nucleotide sequence of a cDNA encoding the T cell surface protein T4: a new member of the immunoglobulin gene family"; Cell 42:93-104(1985).
24	557.5	54.2	474	2	P77355	RX-MADDON, Littman D.R., Godfrey M., Maddon D.B., Chess L., Axel R.; "The isolation and nucleotide sequence of a cDNA encoding the T cell surface protein T4: a new member of the immunoglobulin gene family"; Cell 42:93-104(1985).
25	553	53.7	457	2	Q6GYR3	RX-MADDON, Littman D.R., Godfrey M., Maddon D.B., Chess L., Axel R.; "The isolation and nucleotide sequence of a cDNA encoding the T cell surface protein T4: a new member of the immunoglobulin gene family"; Cell 42:93-104(1985).
26	531	51.6	406	2	Q6J3N3	RX-MADDON, Littman D.R., Godfrey M., Maddon D.B., Chess L., Axel R.; "The isolation and nucleotide sequence of a cDNA encoding the T cell surface protein T4: a new member of the immunoglobulin gene family"; Cell 42:93-104(1985).
27	531	51.6	447	2	Q63N4	RX-MADDON, Littman D.R., Godfrey M., Maddon D.B., Chess L., Axel R.; "The isolation and nucleotide sequence of a cDNA encoding the T cell surface protein T4: a new member of the immunoglobulin gene family"; Cell 42:93-104(1985).
28	488.5	47.5	457	1	CDA_RAT	RX-MADDON, Littman D.R., Godfrey M., Maddon D.B., Chess L., Axel R.; "The isolation and nucleotide sequence of a cDNA encoding the T cell surface protein T4: a new member of the immunoglobulin gene family"; Cell 42:93-104(1985).
29	46.2	457	1	CDA_MOUSE	RX-MADDON, Littman D.R., Godfrey M., Maddon D.B., Chess L., Axel R.; "The isolation and nucleotide sequence of a cDNA encoding the T cell surface protein T4: a new member of the immunoglobulin gene family"; Cell 42:93-104(1985).	
30	45.4	45.4	474	2	Q63J96	RX-MADDON, Littman D.R., Godfrey M., Maddon D.B., Chess L., Axel R.; "The isolation and nucleotide sequence of a cDNA encoding the T cell surface protein T4: a new member of the immunoglobulin gene family"; Cell 42:93-104(1985).
31	42.4	42.4	433	2	Q55054	RX-MADDON, Littman D.R., Godfrey M., Maddon D.B., Chess L., Axel R.; "The isolation and nucleotide sequence of a cDNA encoding the T cell surface protein T4: a new member of the immunoglobulin gene family"; Cell 42:93-104(1985).

## ALIGNMENTS

32	400	38.9	86	2	077596	mandrillus
33	400	38.9	86	2	077597	mandrillus
34	38.5	86	2	077594	cercopithecus	
35	397	38.6	86	2	077599	theropithecus
36	395	38.4	86	2	077595	cercocebus
37	395	38.4	86	2	071655	cercocebus
38	392	38.1	86	2	077598	papio sp. (
39	388	37.7	86	2	077601	lobocebus
40	383	37.2	86	2	077600	lobocebus
41	380	36.9	78	2	061CP8	homo sapien
42	357	34.7	71	2	Q13969	homo sapien
43	305.5	29.7	99	2	Q29027	sus scrofa
44	280.5	27.3	99	2	Q29028	sus scrofa
45	172	16.7	482	2	Q90wbs	anas platyrhynchos

RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,	RT	"Identifi cation or palmitoylation sites on CD4."
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunnarsson P.H.,	RL	J. Biol. Chem. 267:13593-13597(1992).
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	CC	-!- FUNCTION: Accessory protein for MHC class-II antigen/T-cell receptor interaction. May regulate T-cell activation.
RA	Villalon D.K., Muzny D.M., Soderberg B.J., Lu X., Gibbs R.A.,	CC	-!- SUBUNIT: Associates with p56-lck.
RA	Fahy J., Heitton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,	CC	-!- SUBCELLULAR LOCATION: Type I membrane protein. Removed from plasma membrane by HIV-1 Nef protein that increases clathrin-dependent endocytosis of this antigen to target it to lysosomal degradation.
RA	Whiting M., Madan A.C., Shevchenko Y., Bouffard G.G.,	CC	-!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
RA	Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,	CC	-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,	CC	-!- DATABASE: NAME=PROW; NOTE=CD4 guide CD4 entry; WWW="http://www.ncbi.nlm.nih.gov/procd/cd4.htm".
RA	Butterfield Y.M., Krzywinski M.I., Skaluba U., Smailus D.B.,	CC	
RA	Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.,	CC	
RA	"Generation and initial analysis of more than 15,000 full-length human	CC	
RT	and mouse cDNA sequences";	CC	
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	CC	
RN	[6] [16]	CC	
RP	SEQUENCE OF 28-424 FROM N.A.	CC	
RC	TISSUE=BLOOD;	CC	
RX	MEDLINE=93049640; PubMed=4425921;	CC	
RA	Fomsgaard A., Hirsch V.M., Johnson P.R.,	CC	
RT	"Cloning and sequences of primate CD4 molecules: diversity of the cellular receptor for simian immunodeficiency virus/human immunodeficiency virus,"	CC	
RT	Bur. J. Immunol. 22:2973-2981(1992).	CC	
RL	[7]	CC	
RN	SEQUENCE OF 26-394, AND DISTURFIDE BOND.	CC	
RX	MEDLINE=90078232; PubMed=252374;	CC	
RA	Carre S.A., Henning M.E., Folena Wasserman G., Sweet R.W., Anumula K.,	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation of the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
RA	Barr J.K., Hudleston W.J., Taylor P.,	CC	
RT	"Protein and carbohydrate structural analysis of a recombinant soluble CD4 receptor by mass spectrometry,"	CC	
RT	CD4 receptor by mass spectrometry,"	CC	
RL	J. Biol. Chem. 264:21286-21295(1989).	CC	
RN	[8]	CC	
RP	SEQUENCE OF 26-40.	CC	
RX	MEDLINE=1334011; PubMed=101110; ps.04682504;	CC	
RA	Zhang Z., Hensel W.J.,	CC	
RT	"Signal peptide prediction based on analysis of experimentally verified cleavage sites,"	CC	
RT	protein Sci. 13:2819-2824(2004).	CC	
RL	[9]	CC	
RN	REMOVAL FROM CELL SURFACE BY HIV-1 NEF, AND MUTAGENESIS OF MET-432;	CC	
RP	SER-433; 438-LEU-LEU-439 AND SER-440.	CC	
RX	MEDLINE=8124721;	CC	
RA	Aiken C., Konner J., Landau N.R., Lenburg M.E., Trono D.,	CC	
RT	"Nef induces CD4 endocytosis: requirement for a critical dileucine motif in the membrane-proximal CD4 cytoplasmic domain,"	CC	
RL	Cell 76:853-864(1994).	CC	
RN	[10]	CC	
RP	X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 26-208.	CC	
RX	MEDLINE=91061881; PubMed=1701030; DOI=10.1038/348411a0;	CC	
RA	Wang J., Yan Y., Garrett T.P., Liu J., Rodgers D.W., Garlick R.L.,	CC	
RA	Tarz G.E., Husain Y., Reinherz E.L., Harrison S.C.,	CC	
RT	"Atomic structure of a fragment of human CD4 containing two immunoglobulin-like domains,"	CC	
RL	Nature 348:411-418(1990).	CC	
RN	[11]	CC	
RP	X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 26-208.	CC	
RX	MEDLINE=91063882; PubMed=2247146; DOI=10.1038/348419a0;	CC	
RA	Yiu S.-E., Kong P.D., Truneh A., Porter T.G., Arthos J.,	CC	
RA	Rosenberg M., Dai X., Xiong N.-H., Axel R., Sweet R.W.,	CC	
RA	Hendrickson W.A.;	CC	
RT	"Crystal structure of an HIV-binding recombinant fragment of human CD4,"	CC	
RL	Nature 348:419-426(1990).	CC	
RT	CD4; "Dimeric association and segmental variability in the structure of human CD4,"	CC	
RT	dimeric association and segmental variability in the structure of human CD4,"	CC	
RT	Nature 387:527-530(1997).	CC	
RL	[13]	CC	
RP	PALMITOYLATION.	CC	
RX	MEDLINE=92317038; PubMed=1618861;	CC	
RA	Craig R., Rose J.K.;	CC	
RT		CC	
RL		CC	
RN		CC	
RP	X-RAY CRYSTALLOGRAPHY (3.9 ANGSTROMS) OF 26-388.	CC	
RX	MEDLINE=97314402; PubMed=9168119;	CC	
RA	Wu H., Kong P.D., Hendrickson W.A.,	CC	
RT	"Dimeric association and segmental variability in the structure of human CD4,"	CC	
RT	Nature 387:527-530(1997).	CC	
RL	[13]	CC	
RP	PALMITOYLATION.	CC	
RX	MEDLINE=92317038; PubMed=1618861;	CC	
RA	Craig R., Rose J.K.;	CC	
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FT	DOMAIN	26	125	Ig-like V-type.
FT	DOMAIN	126	203	Ig-like C2-type 1.
Query Match		99.4%	Score 1023; DB 1; Length 458;	
Best Local Similarity		99.5%	Pred. No. 3. 5e-77; Pred. No. 3. 5e-77; 0; Mismatches 1; Indels 0; Gaps 0;	
Matches		199;	Conservative	
QY	1	MARGVPRFLILVLQLALLPATOQNKVVLGKGDTWELTCASQKSIQFWKNSNQIK	60	
DR	1	MARGVPRFLILVLQLALLPATOQNKVVLGKGDTWELTCASQKSIQFWKNSNQIK	60	
QY	61	IIGNQSFLTKPSKUNDRAEDRSRSLWDQGNFPLIINKLKIEDSDTYCVDQKERVQL	120	
DR	61	IIGNQSFLTKPSKUNDRAEDRSRSLWDQGNFPLIINKLKIEDSDTYCVDQKERVQL	120	
Db	121	LVFGLTANSDFLHQSOSTITLESPPGSSPSVOCSPRGKNIQGKTLVSOLEQDSG	180	
Db	121	LVFGLTANSDFLHQSOSTITLESPPGSSPSVOCSPRGKNIQGKTLVSOLEQDSG	180	
QY	181	TWCTCTVQONQKVEFKDIV	200	
DR	181	TWCTCTVQONQKVEFKDIV	200	
<b>RESULT 2</b>				
ID	CD4_PANTR	STANDARD;	PRT;	458 AA.
AC	P16004;			
DT	01-APR-1990 (Rel. 14, Created)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	T-cell surface glycoprotein CD4 precursor (T-cell surface antigen			
GN	Name=CD4			
OS	Ban troglopytes (Chimpanzee); Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan. OC			
OC	OCX; TAXID=9598;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90182664; PubMed=2107024; DOI=10.1016/0092-8674(90)90089-W;			
RA	Camerini D.; Seed B.; Cell 60:747-754(1990).			
RP	SEQUENCE OF 26-424 FROM N.A.			
RC	TISSUE=Blood;			
RX	MEDLINE=93049640; PubMed=1425921;			
RA	Fomsgaard A.; Hirsch V.M.; Johnson P.R.; RT			
RT	"Cloning and sequences of primate CD4 molecules: diversity of the cellular receptor for simian immunodeficiency virus/human immunodeficiency virus." [J Immunol. 22:2973-2981(1992). Bur J. Immunol. 22:2973-2981(1992). RL			
CC	-- FUNCTION: Accessory protein for MHC class-II antigen/T-cell receptor interaction. May regulate T-cell activation.			
CC	-- SUBUNIT: Associates with p56-lck (BY similarity).			
CC	-- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.			
CC	-- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
DR	GO; GO:0042101; C-T-cell receptor complex; ISS.			
DR	GO; GO:0015026; F:coreceptor activity; ISS.			
DR	GO; GO:0002289; F:MHC class II protein binding; ISS.			
DR	GO; GO:005955; P:immune response; ISS.			
DR	GO; GO:004086; P:positive regulation of interleukin-2 biosyn. . ; ISS.			
DR	GO; GO:00217; P:T-cell differentiation; ISS.			
DR	GO; GO:004505; P:T-cell selection; ISS.			
DR	GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . ; ISS.			
DR	InterPro; IPR00424; CD2.			
DR	InterPro; IPR00973; CD4_TCR.			
DR	InterPro; IPR00110; Ig-like.			
DR	InterPro; IPR01596; Ig V.			
DR	Pfam; PF00047; Ig; 2.			
DR	PRINTS; PRO0692; CD4_CANTIGEN.			
DR	SMART; SM00406; IgV; 1.			
DR	PROSITE; PS50835; Ig-LIKE; 1.			
KW	Glycoprotein; Immune response; Immunoglobulin domain; Lipoprotein; Palmitate; Repeat; Signal; T-cell; Transmembrane.			
FT	SIGNAL	1	25	By similarity.
FT	CHAIN	26	458	T-cell surface glycoprotein CD4.
FT	TRANSMEM	26	396	N-linked (GlcNAc. . . )
FT	DOMAIN	419	418	Extracellular (Potential).
FT	DISULFID	41	109	Potential.
FT	DISULFID	155	184	Cytoplasmic (Potential).
FT	DISULFID	318	317	Ig-like V-type.
FT	DISULFID	318	374	Ig-like C2-type 1.
FT	CARBOND	296	296	Ig-like C2-type 2.
FT	CARBOND	325	325	Ig-like C2-type 3.
FT	DISULFID	328	370	N-linked (GlcNAc. . . )
FT	LIPID	419	419	By similarity.
FT	LIPID	422	422	S-palmitoyl cysteine (By similarity).
FT	CONFFLICT	42	42	T -> N (in Ref. 2).
FT	CONFFLICT	62	62	L -> S (in Ref. 2).
FT	SEQUENCE	191	191	K -> N (in Ref. 2).
FT	SEQUENCE	458 AA;	51057 MW;	A7C3AC8A5257D3AD CRC64;
Query Match		97.1%	Score 999; DB 1; Length 458;	
Best Local Similarity		97.5%	Pred. No. 3. 6e-75; Pred. No. 3. 6e-75; 0; Mismatches 5; Indels 0; Gaps 0;	
Matches		195;	Conservative	
QY	1	MARGVPRFLILVLQLALLPATOQNKVVLGKGDTWELTCASQKSIQFWKNSNQIK	60	
DR	1	MARGVPRFLILVLQLALLPATOQNKVVLGKGDTWELTCASQKSIQFWKNSNQIK	60	
QY	61	IIGNQSFLTKPSKUNDRAEDRSRSLWDQGNFPLIINKLKIEDSDTYCVDQKERVQL	120	
DR	61	IIGNQSFLTKPSKUNDRAEDRSRSLWDQGNFPLIINKLKIEDSDTYCVDQKERVQL	120	
QY	121	LVFGLTANSDFLHQSOSTITLESPPGSSPSVOCSPRGKNIQGKTLVSOLEQDSG	180	
DR	121	LVFGLTANSDFLHQSOSTITLESPPGSSPSVOCSPRGKNIQGKTLVSOLEQDSG	180	
QY	181	TWCTCTVQONQKVEFKDIV	200	
DR	181	TWCTCTVQONQKVEFKDIV	200	
<b>RESULT 3</b>				
ID	CD4_MACFA	STANDARD;	PRT;	458 AA.
AC	P79185;			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DR	05-JUN-2004 (Rel. 44, Last annotation update)			
DE	T-cell surface glycoprotein CD4 precursor (T-cell surface antigen			
GN	Name=CD4			
OS	Macaca fascicularis (Crab eating macaque) ( <i>Cynomolgus monkey</i> )			
OC	Mammalia; Butheria; Chordata; Craniata; Vertebrata; Euteleostomi;			

OC	Cercopithecinae; Macaca.
RN	{1} - NCBI_TaxID=9541;
RP	SEQUENCE FROM N A.
RC	TISSUE=Thymocyte;
RA	Tatsuni M.; Yabe M.; Yamada Y.K.; Submitted (FEB-1997) to the EMBL/GenBank/DBJ database <sup>B</sup> .
RL	-I- FUNCTION: Accessory protein for MHC class-II antigen/T-cell receptor interaction. May regulate T-cell activation.
CC	-I- SUBUNIT: Associates with p56-1ck (By similarity).
CC	-I- SUBCELLULAR LOCATION: Type I membrane protein.
CC	-I- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC	-I- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).
CC	EMBL: D63349; BAA09673_1; -
DR	HSSP; P01730; IMBR.
DR	GO; GO:0042101; C:T-cell receptor complex; ISS.
DR	GO; GO:0042289; P:MHC class II protein binding; ISS.
DR	GO; GO:0006355; P:immune response; ISS.
DR	GO; GO:0045086; P:positive regulation of interleukin-2 biosyn. . . ; ISS.
DR	GO; GO:003171; P:T-cell differentiation; ISS.
DR	GO; GO:0045058; P:T-cell selection; ISS.
DR	GO; GO:007169; P:transmembrane receptor protein tyrosine kin. . . ; ISS.
DR	InterPro; IPR08424; CD2.
DR	InterPro; IPR0973; CD4.TC4.
DR	InterPro; IPR07110; Ig_V.
DR	InterPro; IPR03596; Ig_V.
DR	Pfam; PF00047; Ig_2.
DR	PRINTS; PRO0692; CD4TCANTIGEN.
DR	SMART; SM00406; IgV; 1.
DR	PROSITE; PS50835; Ig_LIKE; 1.
KW	Glycoprotein; Immune response; Immunoglobulin domain; Lipoprotein; Palmitate; Repeat; Signal; Transmembrane.
FT	SIGNAL 1 25 BY similarity.
FT	CHAIN 26 458 T-cell surface glycoprotein CD4.
FT	DOMAIN 26 396 Extracellular (Potential).
FT	TRANSMEM 397 418 Potential.
FT	DOMAIN 419 458 Cyttoplasmic (Potential).
FT	DOMAIN 26 125 Ig-like V-type.
FT	DOMAIN 126 203 Ig-like C2-type 1.
FT	DOMAIN 204 317 Ig-like C2-type 2.
FT	DOMAIN 318 374 Ig-like C2-type 3.
FT	CARBHYD 42 42 N-linked (GlcNAc. . . ) (Potential).
FT	CARBHYD 295 296 N-linked (GlcNAc. . . ) (By similarity).
FT	CARBHYD 325 325 N-linked (GlcNAc. . . ) (By similarity).
FT	DISTRIFID 41 109 By similarity.
FT	DISTRIFID 184 370 By similarity.
FT	DISTRIFID 328 370 By similarity.
FT	LIPID 419 419 S-palmitoyl cysteine (By similarity).
FT	LIPID 422 422 S-palmitoyl cysteine (By similarity).
SQ	SEQUENCE 458 AA; 50872 MW; 9105479PBC5GFF7 CRC64;
Query Match	88.6%; Score 912; DB 1; Length 458;
Best Local Similarity	80.0%; Pred. No. 6 8e-68;
Matches	176; Conservative 12; Mismatches 12; Indels 0; Gaps 0;
QY	1 MRGRGVPRHLVLTQLALPAATQGNKVVLGKGKDTVELTCRASKQKSIQFHWNKNSWIK 60
QY	1 MNRRGIPPFRRHLVLTQLALPAATQGNKVVLGKGKDTVELTCRASKQKSIQFHWNKNSWIK 60
Db	1 IIGQNSQSLPLTKGPSKLNDRADRSRRSMDQGNFLILKNUKIRDSDTYCEVEQKEEVOL 120
Db	61 ILIGIQSPLTKPKSLSRDRSKLWQGCSMIIKNUKIRDSDTYCEVEENKEEEL 120
Db	
OY	181 TWTCIVLQVOKVKERKIDIV 200
Db	181 TWTCIVSQQDKTVFHKIDIV 200
QY	121 DVFGITANSDDTHILOGSITLTLSPPGSSPVCRSPGKNTGGKTSVSYQSRBLQDSG 180
Db	121 LVFGITANSDDTHILOGSITLTLSPPGSSPVCRSPGKNTGGKTSVSYQSRBLQDSG 180
OY	
RESULT 4	
ID	CD4_MACFU
ID	CD4_MACFU
STANDARD	
PRT	458 AA.
AC	P73184;
DT	15-JUL-1998 (Rel. 36, Created)
DT	15-JUL-1998 (Rel. 36, Last sequence update)
DT	05-JUL-2004 (Rel. 44, Last annotation update)
DB	T-cell surface glycoprotein CD4 precursor (T-cell surface antigen
GN	Name:CD4;
OS	Macaca fuscata fuscata (Japanese macaque).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC	Cercopithecinae; Macaca.
OX	NCBI_TaxID=9543;
RN	[1] - NCBI_TaxID=9543;
RP	SEQUENCE FROM N A.
RA	Hashimoto O., Tatsuni M.; Submitted (FEB-1997) to the EMBL/GenBank/DBJ database.
RL	-I- FUNCTION: Accessory protein for MHC class-II antigen/T-cell receptor interaction. May regulate T-cell activation.
CC	-I- SUBUNIT: Associates with p56-1ck (By similarity).
CC	-I- SUBCELLULAR LOCATION: Type I membrane Protein.
CC	-I- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC	-I- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).
CC	EMBL: D63348; BAA09672_1; -.
DR	HSSP; P01730; IMBR.
DR	GO; GO:0042101; C:T-cell receptor complex; ISS.
DR	GO; GO:0042289; P:MHC class II protein binding; ISS.
DR	GO; GO:0006355; P:immune response; ISS.
DR	GO; GO:0045086; P:positive regulation of interleukin-2 biosyn. . . ; ISS.
DR	GO; GO:0030217; P:T-cell differentiation; ISS.
DR	GO; GO:0045058; P:T-cell selection; ISS.
DR	GO; GO:007169; P:transmembrane receptor protein tyrosine kin. . . ; ISS.
DR	InterPro; IPR08424; CD2.
DR	InterPro; IPR0973; CD4.TC4.
DR	InterPro; IPR07110; Ig-Like.
DR	InterPro; IPR003596; Ig_V.
DR	PRINTS; PRO0692; CD4TCANTIGEN.
DR	SMART; SM00406; IgV; 1.
DR	PROSITE; PS50835; Ig_LIKE; 1.
KW	Glycoprotein; Immune response; Immunoglobulin domain; Lipoprotein; Palmitate; Repeat; Signal; T-cell; Transmembrane.
FT	SIGNAL 1 25 BY similarity.
FT	CHAIN 26 458 T-cell surface glycoprotein CD4.
FT	DOMAIN 26 396 Extracellular (Potential).
FT	TRANSMEM 397 418 Potential.
FT	DOMAIN 419 458 Ig-like V-type.
FT	DOMAIN 126 203 Ig-like C2-type 1.
FT	DOMAIN 204 317 Ig-like C2-type 2.
FT	DOMAIN 318 374 Ig-like C2-type 3.
FT	CARBHYD 42 42 N-linked (GlcNAc. . . ) (Potential).

PT	CARBONID	296	296	N-linked (GlcNAc. . .) (By similarity).
FT	CARBONYD	325	325	N-linked (GlcNAc. . .) (By similarity).
FT	DISULPID	41	109	By similarity.
FT	DISULFID	155	184	By similarity.
FT	DISULFID	328	370	By similarity.
PT	LIPID	419	419	S-palmitoyl cysteine (By similarity).
FT	LIPID	422	422	S-palmitoyl cysteine (By similarity).
SQ	SEQUENCE	458 AA;	50828 MW;	76B3E7EF0185535 CRC64;
Query Match		88.4%	Score 910; DB 1; Length 458;	
Best Local Similarity		87.5%	Pred. No. 1e-67; Indels 0; Gaps 0;	
Matches		175;	Mismatches 13; Mismatches 12; Indels 0; Gaps 0;	
Db	1	MURGIVPFRLILVQLLPLATGKVKVLKGKDTVELTCASOKSIOFWKNSNQIK 60		
Qy		1	MURGIVPFRLILVQLLPLATGKVKVLKGKDTVELTCASOKSIOFWKNSNQIK 60	
Db	1	MURGIVPFRLILVQLLPLATGKVKVLKGKDTVELTCASOKSIOFWKNSNQIK 60		
Qy		61	IGNOQSFLTKPSKDKNDRASSRSIWDQARPLITNLKEDPSDPTVCEPFDQKERVQ 120	
Db	61	IGIQDQSFLTKPSKDKNDRASSRSIWDQARPLITNLKEDPSDPTVCEPFDQKERVQ 120		
Qy		121	LVFGLTANSITLQLQSLSTLTLSPPGSSPVQCSPRKGKILSVQLELQDSG 180	
Db	121	LVFGLTANSITLQLQSLSTLTLSPPGSSPVQCSPRKGKILSVQLELQDSG 180		
Qy		181	TWCTCTVQNONQKVKEFKDIV 200	
Db	181	TWCTCTVQNONQKVKEFKDIV 200		
<b>RESULT 5</b>				
CD4_MACMU	STANDARD;	PRT;	458 AA.	
ID	CD4 MACMU			
AC	P16033; Q99617;			
DT	01-APR-1990 (Rel. 14. Created)			
DT	28-FEB-2003 (Rel. 41. Last sequence update)			
DE	T-cell surface glycoprotein CD4 precursor (T-cell surface antigen)			
GN	Name=CD4;			
OS	Macaca mulatta (Rhesus macaque)			
OC	Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Breheria; Primates; Catarhini; Cercopithecidae;			
OC	Cercopithecinae; Macaca.			
OX	NCBI_TaxID=9544;			
TA	[1]			
RA	SEQUENCE FROM N.A.			
RX	MEDLINE=90182664; PubMed=2107024; DOI=10.1016/0092-8674(90)90089-W;			
RA	Camerini D., Seed B.;			
RT	"A CD4 domain important for HIV-mediated syncytium formation lies outside the virus binding site."			
RT	Cell 60:747-754 (1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RP	RC TISSUE=Thymocytes;			
RA	Hashimoto O., Tatsumi M.;			
RT	"Molecular cloning and expression of macaque CD4s."			
RT	Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.			
RN	[3]			
RP	SEQUENCE OF 28-424 FROM N.A.			
RP	RC TISSUE=Blood;			
RX	MEDLINE=93049640; PubMed=1425921;			
RA	Fomsgaard A., Hirsch V.M., Johnson P.R.;			
RT	"Cloning and sequences of primate CD4 molecules: diversity of the cellular receptor for simian immunodeficiency virus/human immunodeficiency virus."			
RL	Eur. J. Immunol. 22:2973-2981 (1992).			
RN	[4]			
RP	SEQUENCE OF 107-192 FROM N.A.			
RX	MEDLINE=98320644; PubMed=9656488;			
RA	Harris E.E., Dobell T.R.;			
RT	"Nuclear gene trees and the phylogenetic relationships of the mangabeys (Primates: Papionini)."			
Qy		1	MURGIVPFRLILVQLLPLATGKVKVLKGKDTVELTCASOKSIOFWKNSNQIK 60	
Db		1	MURGIVPFRLILVQLLPLATGKVKVLKGKDTVELTCASOKSIOFWKNSNQIK 60	
RL	Mol. Biol. Evol. 15:892-900 (1998).			
CC	-I- FUNCTION: Accessory protein for MHC class-II antigen/T-cell receptor interaction. May regulate T-cell activation.			
CC	-I- SUBUNIT: Associates with p56-ICK (By similarity).			
CC	-I- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-I- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.			
CC	-I- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.			
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EMBL; M31134; AAA36338.1; -;				
EMBL; D6347; BAA671.1; -;				
DR	EMBL; X7326; CHA1752.1; -;			
DR	EMBL; AP057385; AAC25129.1; -;			
DR	HSSP; P01730; IWRB.			
DR	GO; GO:0042289; F:MC receptor activity; ISS.			
DR	GO; GO:006955; P:immune response; ISS.			
DR	GO; GO:0045086; P:positive regulation of interleukin-2 biosyn. . ; ISS.			
DR	GO; GO:0032017; P:T-cell differentiation; ISS.			
DR	GO; GO:004505; P:T-cell selection; ISS.			
DR	GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . ; ISS.			
DR	InterPro; IPR008424; CD2.			
DR	InterPro; IPR000973; CD4_TCAG.			
DR	InterPro; IPR007110; Ig_Like.			
DR	InterPro; IPR003596; Ig_V.			
DR	Pfam; PF00047; Ig_2.			
DR	PRINTS; PRO0692; CD4_CANTIGEN.			
DR	SMART; SM00406; Ig_V; 1.			
DR	PROSITE; PS50835; Ig_LIKE; 1.			
KW	Glycoprotein; Immune response; Immunoglobulin domain; Lipoprotein; Palmitate; Repeat; Signal; T-cell; Transmembrane.			
FT	SIGNAL	1	25	
FT	CHAIN	26	458	T-cell surface glycoprotein CD4.
FT	DOMAIN	26	396	Extracellular (Potential).
FT	TRANSMEM	397	418	Potential.
FT	DOMAIN	419	458	Cyttoplasmic (Potential).
FT	DOMAIN	26	125	Ig-like V-type.
FT	DOMAIN	126	203	Ig-like C2-type 1.
FT	DOMAIN	204	317	Ig-like C2-type 2.
FT	DOMAIN	318	374	Ig-like C2-type 3.
FT	CARBONYD	296	296	N-linked (GlcNAc. . .) (By similarity).
FT	CARBONYD	325	325	N-linked (GlcNAc. . .) (By similarity).
FT	DISULFID	41	109	By similarity.
FT	DISULFID	155	184	By similarity.
FT	DISULFID	328	370	By similarity.
FT	LIPID	419	419	S-palmitoyl cysteine (By similarity).
FT	LIPID	422	422	S-palmitoyl cysteine (By similarity).
FT	CONFFLICT	42	42	N -> T (in Ref. 1).
FT	CONFFLICT	62	62	L -> S (in Ref. 3).
FT	CONFFLICT	67	67	L -> S (in Ref. 2).
FT	CONFFLICT	169	169	I -> L (in Ref. 2).
FT	CONFFLICT	191	191	K -> N (in Ref. 3).
FT	CONFFLICT	248	248	S -> P (in Ref. 2).
FT	CONFFLICT	265	265	R -> Q (in Ref. 3).
FT	CONFFLICT	349	349	A -> T (in Ref. 2).
SQ	SEQUENCE	458 AA;	50884 MW;	8BB00339FAFEC08 CRC64;
Query Match		87.9%	Score 904; DB 1; Length 458;	
Best Local Similarity		87.0%	Pred. No. 3.2e-67; Indels 0; Gaps 0;	
Matches		174;	Conservative 13; Mismatches 13; Indels 0; Gaps 0;	
Db		1	MURGIVPFRLILVQLLPLATGKVKVLKGKDTVELTCASOKSIOFWKNSNQIK 60	
Qy		1	MURGIVPFRLILVQLLPLATGKVKVLKGKDTVELTCASOKSIOFWKNSNQIK 60	



## us-09-939-537-31\_copy\_1\_200.rup

RX MEDLINE=93149640; PubMed=1425921;  
 RA Fomsgaard A., Hirsch V.M., Johnson P.R.;  
 RT "Cloning and sequences of primate CD4 molecules: diversity of the  
 cellular receptor for simian immunodeficiency virus/human  
 immunodeficiency virus.";  
 RL Eur. J. Immunol. 22:2973-2981(1992).  
 RN [13] SEQUENCE OF 28-424 FROM N.A.  
 RT TISSUE=Peripheral blood;  
 RX MEDLINE=93017879; PubMed=9379478;  
 RA Fomsgaard A., Mueller-Truwin M.C., Diop O., Hansen J., Mathiot C.,  
 Corbet S., Barre-Sinoussi F., Allan J.S.;  
 RT "Relation between phylogeny of African green monkey CD4 genes and  
 their respective simian immunodeficiency virus genes.";  
 RL J. Med. Primatol. 26:120-128(1997).  
 RN [14] SEQUENCE OF 107-192 FROM N.A.  
 RX MEDLINE=93320644; PubMed=9356488;  
 RA Harris R.B., Disotell T.R.;  
 RT "Nuclear genes and the phylogenetic relationships of the  
 mangabeys (Primates: Papionini).";  
 RL Mol. Biol. Evol. 15:892-900(1998).  
 CC -!- FUNCTION: Accessory protein for MHC class-II antigen/T-cell  
 receptor interaction. May regulate T-cell activation.  
 CC -!- SUBUNIT: Associates with p56-lck (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.  
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 or send an email to license@isb-sib.ch).  
 CC  
 CC DR EMBL; D86589; BRA13132.1; -.  
 DR EMBL; X73322; CRA51748.1; -.  
 DR EMBL; AF001226; AAB60873.1; -.  
 DR EMBL; AF001228; AAB60875.1; -.  
 DR EMBL; AF057380; AAC25124.1; -.  
 DR HSSP\_P01730, IWIQ.  
 DR GO; GO:0042101; C:T-cell receptor complex; ISS.  
 DR GO; GO:0015026; F:coceptor activity; ISS.  
 DR GO; GO:0042289; F:MHC class II protein binding; ISS.  
 DR GO; GO:006955; P:immune response; ISS.  
 DR GO; GO:0045086; P:positive regulation of interleukin-2 biosyn. . . ; ISS.  
 DR GO; GO:0030217; P:T-cell differentiation; ISS.  
 DR GO; GO:0045058; P:T-cell selection; ISS.  
 DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . . ; ISS.  
 DR Interpro; IPR008424; CD2.  
 DR Interpro; IPR000973; CD4\_Tcag.  
 DR PFam; PF00047; Ig\_1.  
 DR PROSITE; PRO0692; CD4\_TCANIGEN.  
 DR PROSITE; PS50835; IG\_LIKE\_1.  
 KW Glycoprotein; Immune response; Immunoglobulin domain; Lipoprotein;  
 KW Palmitate; Repeat; Signal; T-cell; Transmembrane.  
 PT SIGNAL\_1 25 By similarity.  
 PT CHAIN 26 458 T-cell surface glycoprotein CD4.  
 PT DOMAIN 26 396 Extracellular (Potential).  
 PT TRANSMEM 397 418 Potential.  
 PT DOMAIN 419 458 Cytoplasmic (Potential).  
 PT DOMAIN 26 125 19-like V-type.  
 PT DOMAIN 126 203 19-like C2-type 1.  
 PT DOMAIN 204 317 Ig-like C2-type 2.  
 PT DOMAIN 318 374 19-like C2-type 3.  
 PT CARBOHYD 42 N-linked (GlcNAc. . . ) (Potential).  
 PT CARBOHYD 281 281 N-linked (GlcNAc. . . ) (Potential).  
 PT CARBOHYD 296 296 N-linked (GlcNAc. . . ) (Potential).  
 PT CARBOHYD 325 325 N-linked (GlcNAc. . . ) (Potential).  
 PT DISULPID 41 109 By similarity.

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RESULT 8

CD4_CERTO	ID	CD4_CERTO	STANDARD	PRT;	397 AA.
AC		008336;			
DT	01-OCT-1996	(Rel. 34, Created)			
DT	01-OCT-1996	(Rel. 34, Last sequence update)			
DR	05-JUL-2004	(Rel. 44, Last annotation update)			
DE		T-cell surface glycoprotein CD4 (T-cell surface antigen T4/Leu-3) (Fragment).			
GN		Name=CD4;			
OS		Cercopithecus torquatus atys (Red-crowned mangabey) (sooty mangabey).			
OC		Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC		Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;			
OC		Cercopithecina; Cercopithecidae.			
OK		NCBI_TaxID=9531;			
RN	[1]	SEQUENCE FROM N.A.			
RC		TISSUE=Blood;			
RX		MEDLINE=93049640; PubMed=1425921;			
RA		Fomsgaard A., Hirsch V.M., Johnson P.R.;			
RT		"Cloning and sequences of primate CD4 molecules: diversity of the cellular receptor for simian immunodeficiency virus/human immunodeficiency virus.";			
RL		Eur. J. Immunol. 22:2973-2981(1992).			
CC		-!- FUNCTION: Accessory protein for MHC class-II antigen/T-cell receptor interaction. May regulate T-cell activation.			
CC		-!- SUBUNIT: Associates with p56-lck (By similarity).			
CC		-!- SUBCELLULAR LOCATION: Type I membrane protein.			
CC		-!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.			
CC		-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.			
CC		This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).			

CC	Name=CD4; OS=Brythrocetus patas (Red guenon) ( <i>Cercopithecus patas</i> ). OC=Bukaryota; RC=Mammalia; OC=Cercopithecoidea; RN=[1]; DR=HSPB1; IWIQ.
DR	GO; GO:0015026; F:coreceptor activity; ISS.
DR	GO; GO:004228; F:IMC class II protein binding; ISS.
DR	GO; GO:0006955; P:immune response; ISS.
DR	GO; GO:0045086; P:positive regulation of interleukin-2 biosyn. . . ; ISS.
DR	GO; GO:0032017; P:T-cell differentiation; ISS.
DR	GO; GO:0045058; P:T-cell selection; ISS.
DR	GO; GO:000169; P:transmembrane receptor protein tyrosine kin. . . ; ISS.
DR	InterPro; IPR00974; CD2.
DR	InterPro; IPR00710; Ig-like.
DR	InterPro; IPR00596; Ig_v.
DR	Pfam; PF00047; Ig; 2.
DR	PRINTS; PRO0692; CD4TCANTIGEN.
DR	SMART; SMO0406; IgV; 1.
KW	Glycoprotein; Immune response; Immunoglobulin domain; Lipoprotein; Palmitate; Repeat; T-cell; Transmembrane.
FT	NON_TER 1
FT	DOMAIN <1 359
FT	TRANSMEM 370
FT	CARBOHYD 392
FT	DOMAIN <1 98
FT	DOMAIN 99 176
FT	DOMAIN 177 290
FT	DISULFID 291
FT	CARBOHYD 15 269
FT	LIPID 395
FT	VARIANT 20 43
FT	VARIANT 85 86
FT	VARIANT 96 96
FT	VARIANT 173 173
FT	VARIANT 315 316
FT	NON_TER 397 397
SQ	397 AA; 3926 MW; 8660B636D2DB38A7 CRC64;
Query Match	75.2%; Score 784; DB 1; Length 397;
Best Local Similarity	87.3%; Pred. No. 2.9e-57;
Matches	151; Conservative 11; Mismatches 11; Indels 0; Gaps 0;
QY	28 VVAGKKGDTIVELCTASOKKSIOPHWKNSNQIKTGNQSFLLTKPSKLNDRDSRRSLW 87
Db	1 VVAGKKGDTIVELCTASOKKSIOPHWKNSNQIKTGNQSFLLTKPSKLNDRDSRRSLW 60
QY	88 DQGNPLITKLNKIEDSDTYICEVEDQKEVQVLLVQLGTLANSQDTHLQGQSLTTLQESPP 147
Db	61 DQGCPMSMIKKIIEDESPYICVENKKEVELVFGTANSQDTHLQGQSLTTLQESPP 120
QY	148 GSSISVQCRSPRGKNIQSGKTLSVSQFLQDGTWTCLVQMKQKFKIDV 200
Db	121 GSSPSVKCRSPRGKNIQSGKTLSVSQFLQDGTWTCLVQMKQKFKIDV 173
RESULT 9	
CDA_ERYPAA	STANDARD; PRT; 397 AA.
ID	
AC	Q08739; 01-FEB-1995 (Rel. 31, Last sequence update)
DT	01-FEB-1995 (Rel. 31, Last sequence update)
DT	05-JUL-2004 (Rel. 44, Last annotation update)
DE	T-cell surface glycoprotein CD4 (T-cell surface antigen T4/Leu-3) (Fragment).
Query Match	76.1%; Score 783; DB 1; Length 397;
Best Local Similarity	86.7%; Pred. No. 3.5e-57;
Matches	150; Conservative 10; Mismatches 13; Indels 0; Gaps 0;
QY	28 VVAGKKGDTIVELCTASOKKSIOPHWKNSNQIKTGNQSFLLTKPSKLNDRDSRRSLW 87

## us-09-939-537-31\_copy\_1\_200.rup

RESULT 10

1 VVIGKKGDTVELTCTNASQNTTQFHWNQNQTKLKGKGSFLTKGPSKLDRDLSRSLW 60  
 ID 009261 PRELIMINARY; PRT; 397 AA.  
 AC 009261; Name=CD4;  
 DT 01-JUL-1997 (TREMBrel. 04, Created)  
 DT 01-JUN-1997 (TREMBrel. 04, Last sequence update)  
 DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)  
 DE CD4 (Fragment).  
 GN Name=CD4;  
 OS Cercopithecus tantalus.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
 Cercopithecinae; Cercopithecus.  
 OK NCBI\_TaxID=60712;  
 RN [1]  
 RP SOURCE FROM N.A.  
 RK MEDLINE=98017877; PubMed=9379478;  
 RA Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., Mathiot C., Corbet S., Barre-Sinoussi F., Allan J.S.;  
 RT "Relation between phylogeny of African green monkey CD4 genes and their respective simian immunodeficiency virus genes.", J. Med. Primatol. 26:120-128(1997).  
 DR EMBL; AF001221; HAB60868.1; -.  
 DR HSSP; P01730; IWIQ.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98017879; PubMed=9379478;  
 RA Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., Mathiot C., Corbet S., Barre-Sinoussi F., Allan J.S.;  
 RT "Relation between phylogeny of African green monkey CD4 genes and their respective simian immunodeficiency virus genes.", J. Med. Primatol. 26:120-128(1997).  
 RL BMBL; AF001225; AAB60872.1; -.  
 DR HSSP; P01730; IWIQ.  
 DR GO:0016021; C:integral to membrane; IEA.  
 DR GO:000155; P:cell adhesion; IEA.  
 DR InterPro; IPR00424; CD2.  
 DR InterPro; IPR000973; CD4 TCAG.  
 DR InterPro; IPR00710; Ig-Iike.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00590; C2-set; 2.  
 DR Prints; PRO0692; CD4TCANTIGEN.  
 DR SMART; SM0406; IgV; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 1.  
 FT NON\_TER 397 397  
 SQ SEQUENCE 397 AA; 43954 MW; CF7F2F5D82335B0D CRC64;

Query Match 74.5%; Score 767; DB 2; Length 397;  
 Best Local Similarity 85.5%; Pred. No. 7\_6e-56; Pct. Gaps 0;  
 Matches 148; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

Query 28 VVIGKKGDTVELTCTASQKKSTQFHWNQNQTKLKGKGSFLTKGPSKLDRDLSRSLW 87  
 ID 009263 PRELIMINARY; PRT; 397 AA.  
 AC 009263; Name=CD4;  
 DT 01-JUL-1997 (TREMBrel. 04, Created)  
 DT 01-JUL-1997 (TREMBrel. 04, Last sequence update)  
 DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)  
 DE CD4 (Fragment).  
 GN Name=CD4;  
 OS Cercopithecus tantalus.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
 Cercopithecinae; Cercopithecus.  
 OK NCBI\_TaxID=60712;  
 RN [1]  
 RP SOURCE FROM N.A.  
 RX MEDLINE=98017879; PubMed=9379478;  
 RA Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., Mathiot C., Corbet S., Barre-Sinoussi F., Allan J.S.;  
 RT "Relation between phylogeny of African green monkey CD4 genes and

RESULT 11

009262 PRELIMINARY; PRT; 397 AA.

RESULT 12

1 VVIGKKGDTVELTCTASQKKSTQFHWNQNQTKLKGKGSFLTKGPSKLDRDLSRSLW 60  
 ID 009263 PRELIMINARY; PRT; 397 AA.  
 AC 009263; Name=CD4;  
 DT 01-JUL-1997 (TREMBrel. 04, Created)  
 DT 01-JUL-1997 (TREMBrel. 04, Last sequence update)  
 DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)  
 DE CD4 (Fragment).  
 GN Name=CD4;  
 OS Cercopithecus tantalus.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
 Cercopithecinae; Cercopithecus.  
 OK NCBI\_TaxID=60712;  
 RN [1]  
 RP SOURCE FROM N.A.  
 RX MEDLINE=98017879; PubMed=9379478;  
 RA Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., Mathiot C., Corbet S., Barre-Sinoussi F., Allan J.S.;  
 RT "Relation between phylogeny of African green monkey CD4 genes and

RT their respective simian immunodeficiency virus genes.";

RL J. Med. Primatol. 26:120-128(1997).

DR EMBL; AF001227; AAB60869.1; -.

DR HSSP; P01730; IWIQ.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0006955; P:immune response; IEA.

DR InterPro; IPR008424; CD2.

DR InterPro; IPR00973; CD4 TCAG.

DR InterPro; IPR007110; Ig-Like.

DR Pfam; PF005790; C2-set; 2.

DR PRINTS; PR00692; CD4TCANTIGEN.

DR PROSITE; PSS0835; IG\_LIKE; 1.

FT NON\_TER 1

SQ SEQUENCE 397 AA; 43894 MW; A3CD031535A51524 CRC64;

Query Match 74.5%; Score 767; DB 2; Length 397;  
Best Local Similarity 85.5%; Pred. No. 7.6e-56;  
Matches 148; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 28 VVLGKKGDTVELTCTASQKKS1QFHWKNSNQIKILGNQGSFLTKGPSKLNRADRSRSLW 87  
1 VVLGKKGDTVELTCTASQKKS1QFHWKNSNQIKILGNQGSFLTKGPSKLNRADRSRSLW 60

QY 88 DQGNPLIKNLKEBDSDTYCIEVEDQKEREVOLVFLGFTANSQHLLQGQSTLTESPP 147  
1 DQGNPLIKNLKEBDSDTYCIEVEDQKEREVOLVFLGFTANSQHLLQGQSTLTESPP 120

Db 61 DQGFSMIIKNLKIEDSETTYCIEVENKKEBEVELLVFGITVANSQHLLQGQSTLTESPP 120

QY 148 GSSPSVQCRSPRGKNIQGKTLVSQLEHQDGTWTCTVLQNRKVERKIDIV 200  
121 GSPPSVKCRSPRGKNIQGKTLVSQLEHQDGTWTCTVSDQNTVEFKIDIV 173

RESULT 13

Q95N99 PRELIMINARY; PRT; 397 AA.

ID Q95N99 ID: Q95N99; Name=CD4; OC Mammalia; OX NCBI\_TaxID=60710; RN [1]—

RR SEQUENCE FROM N.A.

RX MEDLINE=98017879; PubMed=9379478;

RA Fomsaard A., Muller-Trutwin M.C., Diop O., Hansen J., Mathiot C., Corbet S., Barre-Sinoussi P., Allan J.S.; DR EMBL; AF001223; AAB60870.1; -.

RT "Relation between phylogeny of African green monkey CD4 genes and their respective simian immunodeficiency virus genes"; DR J. Med. Primatol. 26:120-128(1997).

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0007155; P:cell adhesion; IEA.

DR InterPro; IPR008424; CD2.

DR InterPro; IPR00973; CD4 TCAG.

DR InterPro; IPR007110; Ig-Like.

DR Pfam; PF005790; C2-set; 2.

DR PRINTS; PR00692; CD4TCANTIGEN.

DR PROSITE; PSS0835; IG\_LIKE; 1.

FT NON\_TER 1

SQ SEQUENCE 397 AA; 43881 MW; TCB39ADDP8506C81 CRC64;

Query Match 74.1%; Score 763; DB 2; Length 397;  
Best Local Similarity 85.0%; Pred. No. 1.7e-55;  
Matches 147; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 28 VVLGKKGDTVELTCTASQKKS1QFHWKNSNQIKILGNQGSFLTKGPSKLNRADRSRSLW 87  
1 VVLGKKGDTVELTCTASQKKS1QFHWKNSNQIKILGNQGSFLTKGPSKLNRADRSRSLW 60

QY 88 DQGNPLIKNLKEBDSDTYCIEVEDQKEREVOLVFLGFTANSQHLLQGQSTLTESPP 147  
1 DQGNPLIKNLKEBDSDTYCIEVEDQKEREVOLVFLGFTANSQHLLQGQSTLTESPP 120

RESULT 15

Ov 148 GSPSVQCRSPKNIQGKTTSVQLQPSCTWTCNLQPKKKVERKIDIV 200  
 ID 009260 PRELIMINARY; PRT; 397 AA.  
 AC 009260;  
 DT 01-JUL-1997 (TREMBLE1; 04; Created)  
 DT 01-OCT-2003 (TREMBLE1; 04; Last sequence update)  
 DT 01-OCT-2003 (TREMBLE1; 25; Last annotation update)  
 DR CD4 (fragment).  
 DR Name=CD4;  
 OS Cercopithecus sabaeus.  
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidæ;  
 OC Cercopithecinae; Cercopithecus.  
 OX NCBI\_TAXID=60711;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98017879; PubMed=9379478;  
 RA Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., Mathiot C.,  
 RA Corbett S., Barre-Sinoussi F., Allian J.S.;  
 RT "Relation between phylogeny of African green monkey CD4 genes and  
 their respective simian immunodeficiency virus genes.";  
 RL J. Med. Primatol. 26:120-128 (1997).  
 DR EMBL; AF001224; AAB60871.1; -.  
 DR HSSP; P01730; INI0Q.  
 DR GO; GO:001021; C:integral to membrane; IEA.  
 DR GO; GO:0007155; P:cell adhesion; IEA.  
 DR GO; GO:000955; P:immune response; IEA.  
 DR InterPro; IPR008424; CD2.  
 DR InterPro; IPR00973; CD4\_TCAG.  
 DR InterPro; IPR07110; Ig-Like.  
 DR InterPro; IPR03596; Ig\_V.  
 DR Pfam; PF00790; C2-set; 2.  
 DR Pfam; PF00047; Ig; 1.  
 DR PRINTS; PRO0692; CD4CANTIGEN.  
 DR SMART; SM00406; IgV; 1.  
 DR PROSITE; PS50835; IG-LIKE; 1.  
 PT NON\_TER 1  
 FT 397 AA; 397  
 SQ SEQUENCE 397 AA; 43882 MW; 478BB277E992BE89 CRC64;  
 Query Match 74.1%; Score 763; DB 2; Length 397;  
 Best Local Similarity 85.0%; Pred. No. 1; 7e-55;  
 Matches 147; Conservative 11; Mismatches 15; Indels 0; Gaps 0;  
 QY 28 VVLGKKGDTVELCTCTASOKSIQPHWKNSNQIKLGNQGSFJKGPSKNDADRSRSLW 87  
 Db 1 VVLGKKGDTVELCTCTASOKSIQPHWKNSNQIKLGNQGSFJKGPSKNDADRSRSLW 60  
 QY 88 DQDNFLPLTKNIKIEDSDPTTVERVEDOKEEVLDLVLFGLTANDDTHLQGQSTLTLESPP 147  
 Db 61 DQGCFSMILKNIKIEDSDPTTVERVEDOKEEVLDLVLFGLTANDDTHLQGQSTLTLESPP 120  
 Qy 148 GSPSVQCRSPKNIQGKTTSVQLQPSCTWTCNLQPKKKVERKIDIV 200  
 Db 121 GSPSVQCRSPKNIQGKTTSVQLQPSCTWTCNLQPKKKVERKIDIV 173

Search completed: March 7, 2005, 07:19:30  
 Job time : 75.9095 secs

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